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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Mark Spencer

Timestamp: Wed May 16 16:15:29 EDT 2007

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Reviewer Comments:

E253 The number of bases differs from <211> Input: 12 Calculated:17 SEQID (6710511)

<400> 6710511
catatacctc tt <211> 22
<212> DNA
<213> Homo sapiens

<400> 6710519
catatagcat tgataatctt ca 22

Fix – Change the number of bases to the right of sequence for 6710511 to 12.
Missing SEQ ID # 6710512 to complete SEQ ID # 6710519.

E253 The number of bases differs from <211> Input: 22 Calculated:24 SEOID (9319192)

```
<400> 9319192
aatgaaatga agatatgatc ag          1> 22
<212> DNA
<213> Homo sapiens
```

<400> 9319201
aatgcagtga gccattaaat gg 2

Fix – Change the number of bases to the right of sequence for 9319192 to 22.

Missing SEQ ID # 9319193 to complete SEQ ID # 9319201.

E202 Invalid input format; Value must be an integer in <210> in SEQID (9974642)
E249 Order Sequence Error <210> -> <213>; Expected Mandatory Tag: <211> in SEQID
(9974642)

<210> 9974642

<211> 22

<212> DNA

<213> Homo sapiens

<400> 9974642

tctcagggct cagagctcag gc 22

<210> 9972> DNA

<213> Homo sapiens

<400> 9974651

tctctgccca ctgcttccca tt 22

Fix – Missing SEQ ID # 9974643 to complete SEQ ID # 9974651.

E254 The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID
(10068324)

E253 The number of bases differs from <211> Input: 18 Calculated:20 SEQID (10068324)

This is OK no fix is required.

E252 Calc# of Seq. differs from actual; 10068324 seqIds defined; count=10068237

Fix – Numeric Identifier <160> says there is a total of 10068324 sequences. The computer only counted 10068237.

Provide the missing sequences above or adjust the numbering of the sequences and change <160> to reflect the actual total.

Application No: 10709572

Version No: 1.0

Started: 2007-04-26 15:09:46.706

Finished: 2007-04-26 18:23:53.100

Elapsed: 3 hr(s) 14 min(s) 6 sec(s) 394 ms

Total Warnings: 0

Total Errors: 75

No. of SeqIDs Defined: 10068324

Actual SeqID Count: 10068237

ErrCode	Error Description
E 212	Invalid Sequence ID Number; Expected 165602 as next SeqID but skipped to 165603
E 212	Invalid Sequence ID Number; Expected 329702 as next SeqID but skipped to 329703
E 212	Invalid Sequence ID Number; Expected 493802 as next SeqID but skipped to 493803
E 212	Invalid Sequence ID Number; Expected 657902 as next SeqID but skipped to 657903
E 212	Invalid Sequence ID Number; Expected 822002 as next SeqID but skipped to 822003
E 212	Invalid Sequence ID Number; Expected 986102 as next SeqID but skipped to 986103
E 212	Invalid Sequence ID Number; Expected 1148302 as next SeqID but skipped to 1148303
E 212	Invalid Sequence ID Number; Expected 1310302 as next SeqID but skipped to 1310303
E 212	Invalid Sequence ID Number; Expected 1472302 as next SeqID but skipped to 1472303
E 212	Invalid Sequence ID Number; Expected 1634302 as next SeqID but skipped to 1634303
E 212	Invalid Sequence ID Number; Expected 1796302 as next SeqID but skipped to 1796303
E 212	Invalid Sequence ID Number; Expected 1958302 as next SeqID but skipped to 1958303
E 212	Invalid Sequence ID Number; Expected 2120302 as next SeqID but skipped to 2120303
E 212	Invalid Sequence ID Number; Expected 2282302 as next SeqID but skipped to 2282303

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Total Warnings: 0
Total Errors: 75
No. of SeqIDs Defined: 10068324
Actual SeqID Count: 10068237

ErrCode	Error Description
E 212	Invalid Sequence ID Number; Expected 2444302 as next SeqID but skipped to 2444303
E 212	Invalid Sequence ID Number; Expected 2606302 as next SeqID but skipped to 2606303
E 212	Invalid Sequence ID Number; Expected 2768302 as next SeqID but skipped to 2768303
E 212	Invalid Sequence ID Number; Expected 2930302 as next SeqID but skipped to 2930303
E 212	Invalid Sequence ID Number; Expected 3092302 as next SeqID but skipped to 3092303
E 212	Invalid Sequence ID Number; Expected 3254302 as next SeqID but skipped to 3254303 This error has occurred more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total, Input: 22, Calculated : 17 SEQID(6710511)
E 253	The number of bases differs from <211> Input: 12 Calculated:17 SEQID (6710511)
E 254	The total number of bases conflicts with running total, Input: 22, Calculated : 24 SEQID(9319192)
E 253	The number of bases differs from <211> Input: 22 Calculated:24 SEQID (9319192)
E 202	Invalid input format; Value must be an integer in <210> in SEQID (9974642)
E 249	Order Sequence Error <210> -> <213>; Expected Mandatory Tag: <211> in SEQID (9974642)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID(10068324)
E 253	The number of bases differs from <211> Input: 18 Calculated:20 SEQID (10068324)
E 252	Calc# of Seq. differs from actual; 10068324 seqIds defined; count=10068237
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> ROSETTA GENOMICS LTD

Bentwich, Itzhak

Avniel, Amir

<120> BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
OLIGONUCLEOTIDES AND USES THEREOF

<130> 050992.0202.CPUS01

<140> 10/709,572

<141> 2004-05-14

<160> 10068324

<170> PatentIn version 3.3

<210> 1

<211> 17

<212> DNA

<213> Homo sapiens

<400> 1

gcgcctgtgc ctcttaa

17

<210> 2

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2

gctccactg ctgtctgcc at

22

<210> 3

<211> 22

<212> DNA

<213> Homo sapiens

<400> 3

gctgcacttc agcctgggtg tc 22

<210> 4
<211> 22
<212> DNA
<213> Homo sapiens

<400> 4
gctggctcca cctgctgcca gg 22

<210> 5
<211> 21
<212> DNA
<213> Homo sapiens

<400> 5
ggaatgggtg ttgatggtt g 21

<210> 6
<211> 23
<212> DNA
<213> Homo sapiens

<400> 6
ggccaagtgg atgctggttt agc 23

<210> 7
<211> 22
<212> DNA
<213> Homo sapiens

<400> 7
ggccgggtgc tctggagtg ct 22

<210> 8
<211> 22
<212> DNA
<213> Homo sapiens

<400> 8
ggccgtggtc gctgactctc gt 22

<210> 9
<211> 22
<212> DNA
<213> Homo sapiens

<400> 9
ggctggtag atttggtc tt 22

<210> 10
<211> 22
<212> DNA
<213> Homo sapiens

<400> 10
gggaataat taatgtgaag tc 22

<210> 11
<211> 22
<212> DNA
<213> Homo sapiens

<400> 11
ggggaacgcg ctggcccgcg cc 22

<210> 12
<211> 19
<212> DNA
<213> Homo sapiens

<400> 12
gggtctctgt tggcttctt 19

<210> 13
<211> 22

<212> DNA
<213> Homo sapiens

<400> 13
gggttactct gtgttgggtca gg 22

<210> 14
<211> 22
<212> DNA
<213> Homo sapiens

<400> 14
ggtggcccct gggagatgct gg 22

<210> 15
<211> 22
<212> DNA
<213> Homo sapiens

<400> 15
gtcagtcatt gaatgctggc ct 22

<210> 16
<211> 22
<212> DNA
<213> Homo sapiens

<400> 16
gtgcggccctg gccctcaagt gg 22

<210> 17
<211> 22
<212> DNA
<213> Homo sapiens

<400> 17
gtgcttaaag aatggctgtc cg 22

<210> 18
<211> 19
<212> DNA
<213> Homo sapiens

<400> 18
gtttctctgg gcttggcat 19

<210> 19
<211> 20
<212> DNA
<213> Homo sapiens

<400> 19
tagcatggct ctatggaaca 20

<210> 20
<211> 22
<212> DNA
<213> Homo sapiens

<400> 20
taggtatggc ttgtggcaca gc 22

<210> 21
<211> 22
<212> DNA
<213> Homo sapiens

<400> 21
tattcattgc ccatgtttgt ga 22

<210> 22
<211> 22
<212> DNA
<213> Homo sapiens

<400> 22
tcaactgcaac ctccaccttc ag 22

<210> 23
<211> 22
<212> DNA
<213> Homo sapiens

<400> 23
tccagctgtc cacgtcttcc tg 22

<210> 24
<211> 23
<212> DNA
<213> Homo sapiens

<400> 24
tccaggccct caatccattt cca 23

<210> 25
<211> 22
<212> DNA
<213> Homo sapiens

<400> 25
tccagctcc tgggccccac ag 22

<210> 26
<211> 22
<212> DNA
<213> Homo sapiens

<400> 26
tccttcctct gtcaggcagg cc 22

<210> 27
<211> 22
<212> DNA
<213> Homo sapiens